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sequences shown in Fig. 1

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7200
7260
7320

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ataacttcgt aaatagtccc aataacagag tactcgccata tgtataaact tacataaatac	8100
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<210> 4
 <211> 2100
 <212> DNA
 <213> Artificial

<220>
 <223> mCEA(6D) sequence shown in Fig. 2A

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acgccgttca atgtcgacaa gggaaaggag gtgtttcac ttgtccacaa tctgccccag	180
catcttttg gctacagctg gtacaaagggt gaaagagtgg atggcaaccg tcaaattata	240
ggatatgtaa taggaactca acaagctacc ccagggccccg catacagtgg tcgagagata	300
atataccccca atgcattccct gctgatccag aacatcatcc agaatgacac aggattctac	360
accctacacg tcataaaagtc agatcttgcg aatgaagaag caactggcca gttccgggtt	420
tacccggaaac tccctaaagcc ttctatttagc tccataata gtaaggctgt cgaagacaaa	480

gatgccgtcg	ctttacatg	cgagccgaa	actcaagacg	caacatatct	ctggtggtg	540
aacaaccagt	ccctgcctgt	gtcccctaga	ctccaactca	gcaacggaaa	tagaactctg	600
accctgttta	acgtgaccag	gaacgacaca	gcaagctaca	aatgcgaaac	ccaaaatcca	660
gtcagcgcca	ggaggtctga	ttagtgcatt	ctcaacgtgc	tttacggacc	cgtgctcct	720
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gccgctagca	atcctcccgc	ccaatacagc	tggttgtca	atggcacttt	ccaacagtcc	840
acccaggaac	tgttcattcc	caatattacc	gtgaacaata	gtggatccta	cacgtgcaa	900
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ccacaaaaac	cattcataac	tagtaacaat	tctaaccag	ttgaggatga	ggacgcagtt	1020
gcattaactt	gtgagccaga	gattcaaaat	accacttatt	tatggtggt	caataaccaa	1080
agtttgcgg	ttagccacg	cttgcagttg	tctaatgata	accgcacatt	gacactcctg	1140
tccgttactc	gcaatgatgt	aggaccttat	gagtgtggca	ttcagaatga	attatccgtt	1200
gatcactccg	accctgttat	ccttaatgtt	ttgtatggcc	cagacgaccc	aactataatct	1260
ccatcataca	cctactaccg	tccggcgtg	aacttgagcc	tttcttgcca	tgcagcatcc	1320
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aagccctcca	tctccagcaa	caactccaaa	cccgtggagg	acaaggatgc	tgtggccttc	1560
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tccccgcagt	attcttggcg	tatcaatggg	ataccgcagc	aacacacaca	agttctttt	1920
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actggccgca	ataattccat	agtcaagagc	atcacagtct	ctgcacatctgg	aacttctcct	2040
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<210> 5
<211> 2100

<212> DNA
 <213> Artificial

 <220>
 <223> mCEA(6D, 1st & 2nd) sequence shown in Fig. 2A

 <400> 5
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 acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
 catcttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
 ggatatgtaa taggaactca acaagctacc ccagggcccg catabactgg tcgagagata 300
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 accctacacg tcataaagtc agatcttgc aatgaagaag caactggcca gttccggta 420
 tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480
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 aacaatcaga gcctcccggt cagtcggagg ctgcagctgt ccaatggcaa caggaccctc 600
 actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
 gtgagtggca ggcgcaigtga ttcaigtcatc ctgaatgtcc tctatggccc ggatgcccc 720
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 gaccacagcg acccagtcat cctgaatgtc ctctatggcc cagacgaccc caccattcc 1260
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aagccctcca	tctccagcaa	caactccaaa	cccgtggagg	acaaggatgc	tgtggcctc	1560
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ccagtcagtc	ccaggctgca	gctgtccaat	ggcaacagga	ccctcactct	attcaatgtc	1680
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tccccgcagt	attcttggcg	tatcaatggg	ataccgcagc	aacacacaca	agttctcttt	1920
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<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6

Leu Leu Thr Phe Trp Asn Pro Pro Thr
1 5

<210> 7
<211> 10
<212> PRT
<213> Homo sapiens

<400> 7

Val Leu Tyr Gly Pro Asp Ala Pro Thr Ile
1 5 10

<210> 8
<211> 9
<212> PRT
<213> Homo sapiens

<400> 8

Ile Met Ile Gly Val Leu Val Gly Val
1 5

<210> 9
<211> 9
<212> PRT

<213> Homo sapiens

<400> 9

Gln Ile Ile Gly Tyr Val Ile Gly Thr
1 5

<210> 10

<211> 9

<212> PRT

<213> Homo sapiens

<400> 10

Lys Thr Cys Pro Val Gln Leu Trp Val
1 5

<210> 11

<211> 9

<212> PRT

<213> Homo sapiens

<400> 11

Ser Thr Pro Pro Pro Gly Thr Arg Val
1 5

<210> 12

<211> 11

<212> PRT

<213> Homo sapiens

<400> 12

Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu
1 5 10

<210> 13

<211> 10

<212> PRT

<213> Homo sapiens

<400> 13

Val Val Val Pro Tyr Glu Pro Pro Glu Val
1 5 10

<210> 14

<211> 314

<212> PRT

<213> Homo sapiens

<400> 14

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Scr Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
260 265 270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 15
<211> 314
<212> PRT
<213> Artificial

<220>
<223> Modified KSA amino acid sequence as shown in Fig. 3

<400> 15

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Asn Gly Ser Lys Leu Gly Arg
65 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
130 135 140

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
145 150 155 160

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
165 170 175

Asp Pro Lys Phe Ile Thr Ser Val Leu Tyr Glu Asn Asn Val Ile Thr
180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
195 200 205

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
210 215 220

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
225 230 235 240

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
245 250 255

Pro Glu Phe Ser Met Gln, Gly Leu Lys Ala Gly Val Ile Ala Val Ile
260 265 270

Val Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile
275 280 285

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu
290 295 300

Met Gly Glu Met His Arg Glu Leu Asn Ala
305 310

<210> 16
<211> 10
<212> PRT
<213> Homo sapiens

<400> 16

Gln Leu Asp Pro Lys Phe Ile Thr Ser Ile
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Amino acid sequence of KSA peptide modified at amino acid 10

<400> 17

Gln Leu Asp Pro Lys Phe Ile Thr Ser Val
1 5 10

<210> 18
<211> 36
<212> DNA
<213> Homo sapiens

<400> 18
caaaaatttat cacgagtgtg ttgtatgaga ataatg 36

<210> 19
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Nucleotide sequence of KSA peptide modified at amino acid 10

<400> 19
cattattctc atacaacaca ctcgtataa attttg 36

<210> 20
<211> 945
<212> DNA
<213> Artificial

<220>
<223> Modified KSA nucleic acid sequence as shown in Fig. 3B

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aataataatc	gtcaatgcca	gtgtacttca	gttgggtcac	aaaataactgt	catttgccta	180
aagctggctg	ccaaatgttt	ggtgatgaag	gcagaaaatga	atggctcaaa	acttgggaga	240
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gagagcgggc	tcttaaggc	caagcagtgc	aacggcacct	ccacgtgctg	gtgtgtgaac	360
actgctgggg	tcagaagaac	agacaaggac	actgaaataa	cctgctctga	gcgagtgaga	420
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caaaaaactc	agaatgatgt	ggacatagct	gatgtggctt	attatttga	aaaagatgtt	660
aaaggtgaat	ccttggttca	ttctaagaaa	atggacctga	cagtaaatgg	ggaacaactg	720
gatctggatc	ctggtcaaacc	tttaatttat	tatgttgatg	aaaaagcacc	tgaattctca	780
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gctggaattg	ttgtgctggt	tatttccaga	aagaagagaa	tggcaaagta	tgagaaggct	900
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<210> 21
<211> 9515
<212> DNA
<213> Artificial

<220>
<223> SENSE strand of plasmid pT225KSAV-1 shown in Fig. 5

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